

Figure 1A

1 CCACGCGTCCGAACATGGGCTGAGAGCCCCCAAGAGCATCTCTAAGACCGGAGTGGGC 60
 61 AGGGACCCGGGCTCTGAGGGGCTCAGGCTCCAGGCCGAAACTGCACGCGGTGCTGGCG 120
 121 TCAGGCCCGAGGCCAGCTACGCCTCCACGGCCTCCCTAATCGCCATTTCGGGGCTTGCG 180
 181 GGAGCACCTGGGAGGCTCCACCCGGAGCCAGACACTGCCTGCCCCACGCCCCCTCCAGGA 240
 241 CCCTCGAAGGAGAAGGAAATCGGGACTGGCCCAGCGTCCCGTGCTCTAGAAGGCGGGCTA 300
 301 CTGCCCCGTCCCAAGCAGGGGAGGAGGACGAGCGAGGGCGTCACTCATTCTGTCCCCCGC 360
 361 GGAAGGATGAGGAAGCTCTGTTTACCTAAATGAAAAGCTTTCTAGGAGGAAGTCCTAAGT 420
 421 GAACAATGATGCATGAGGATGCAATCTTACAGACACAGGGTCTCCCTATGTTGTTCAAG 480
 481 CTGGTCTCGAACTCCTGGCCTCAAGTGATCCTCCTGCCTCGACCTCTCAAAGCTCTGGTA 540
 541 TTATAGGCAAGGAGCCCAGTGATAACAAATGGCTGTAGATGCTTTTCCTCCATCAAGCTT 600
 601 CCAGGAGGAGATGAGATGGAGCCCCATCGCTGAGCCAAGAATTCTAATTTTCATCCCTTTGG 660
 661 TCTTTGTTTCATGCTGTGTTCTGCCTGGAATATTCTCCATCTTCTTTGCCTGGAAAAGTAT 720
 721 TACTTACTGAAACCTTGAAGCCACTACCTTCTCTAAACATTGACAATGCATAACCATTTG 780
 781 CCGAGCGTTCTTCCCCGACTGCATCCGTTTAGTCTACTGAGAGGCAGCTCAGCGTTCCC 840
 841 AAGGAGACAGATGTCTAGCTTTGCTCTTTCTGTCTGTGTGATGCTGGAGAATCGATATGC 900
 901 CCCTGGGCCTCCATCTCCATCTGTAAAACAAGGCATCAGATACCCACCTGGTGGCCCCG 960
 961 TCCTCACTTGGGAACCACTCAACATGCCTTCTGGAAGTCTCTCTTGTCACTCCAAGAAAA 1020
 1021 GATCCCCAGGAAACCTACAGGGACTATGTCCGCAGGAAATTCCGGCTCATGGAAGACCGC 1080
 1081 AATGCGCGCTTAGGGGAATGTGTCAACCTCAGCCACCGGTACACCCGGCTCCTGCTGGTG 1140
 1141 AAGGAGCACTCAAACCCCATGCAGGTCCAGCAGCAGCTTCTGGACACAGGCCGGGGACAC 1200

Figure 1B

1201 GCGAGGACCGTGGGACACCAGGCTAGCCCCATCAAGATAGAGACCCTCTTTGAGCCAGAC 1260

1261 GAGGAGCGCCCCGAGCCACCGCGCACCGTGGTCATGCAAGGCGCGGCAGGGATAGGGAGA 1320
1 M

1321 TGAACCGAGGTGCCACGGAATGCAGCATGCAAGACCTCATCTTCAGCTGCTGGCCTGAGC 1380
2 N Q S A T E C S M Q D I F S C W P E P 21

1381 CCAGCGCGCCTCTCCAGGAGCTCATCCGAGTTCCTCGAGCGCCTCCTTTTCATCATCGACG 1440
22 S A P L Q E L I R V P E R L F I I D G 41

1441 GCTTCGATGAGCTCAAGCCTTCTTCCACGATCCTCAGGACCCCTGGTGCCTCTGCTGGG 1500
42 F D E L K P S F H D P Q G P W C L C W E 61

1501 AGGAGAAACGGCCACGGAGCTGCTTCTTAACAGCTTAATTCGGAAGAAGCTGCTCCCTG 1560
62 E K R P T E L N S I R K K L P E 81

1561 AGCTATCTTTGCTCATCACCACACGGCCCCCGGCTTTGGAGAAGCTCCACCGTCTGCTGG 1620
82 L S L I T T R P T A L E K L H R L E 101

1621 AGCACCCAGGCATGTGGAGATCCTGGGCTTCTCTGAGGCAGAAAGGAAGGAATACTTCT 1680
102 H P R H V E I L G F S E A E R K E Y F Y 121

1681 ACAAGTATTTCCACAATGCAGAGCAGGCGGGCCCAAGTCTTCAATTACGTGAGGGACAACG 1740
122 K Y F H N A E Q A G Q V F N Y V R D N E 141

1741 AGCCTCTCTTACCATGTGCTTCGTCCTCCCTTGGTGTGCTGGGTGGTGTGTACCTGCCTCC 1800
142 P L F T M C F V P L V C W V V C T C L Q 161

1801 AGCAGCAGCTGGAGGGTGGGGGGCTGTTGAGACAGACGTCCAGGACCACCACTGCAGTGT 1860
162 Q Q L E G G G L L R Q T S R T T T A V Y 181

1861 ACATGCTCTACCTGCTGAGTCTGATGCAACCCAAGCCGGGGGGCGCCTCCAGCCCC 1920
182 M L Y L L S L M Q P K P G A P R L Q P P 201

1921 CACCCAACCAGAGAGGGTGTGCTCCTTGGCGGCAGATGGGCTCTGGAATCAGAAAATCC 1980
202 P N Q R G C S L A A D G L W N Q K I L 221

1981 TATTTGAGGAGCAGGACCTCCGGAAGCACGGCCTAGACGGGAAGACGTCTCTGCCTTCC 2040
222 F E E Q D L R K H G D G E D V S A F L 241

2041 TCAACATGAACATCTTCCAGAAGGACATCAACTGTGAGAGGAGCTTCTGGCACTCACCA 2100
242 N M N I F Q K D I N C E R S F L A L T S 261

Figure 1C

2101 GCCGCTTCCTGTTTGGACTCCTGAACGAGGAGACCAGGAGCCACCTGGAGAAGAGTCTCT 2160
 262 R F **E** F G **E** **E** N E E T R S H **L** E K S L C 281
 2161 GCTGGAAGGTCTCGCCGACATCAAGATGGACCTGTTGCAGTGGATCCAAAGCAAAGCTC 2220
 282 W K V S P H I K M D **E** L Q W I Q S K A Q 301
 2221 AGAGCGACGGCTCCACCCTGCAGCAGGGCTCCTTGGAGTCTTTCAGCTGCTTGTACGAGA 2280
 302 S D G S T L Q Q G S **L** E F F S C **L** Y E I 321
 2281 TCCAGGAGGAGGAGTTTATCCAGCAGGCCCTGAGCCACTTCCAGGTGATCGTGGTCAGCA 2340
 322 Q E E E F I Q Q A L S H F Q V I V V S N 341
 2341 ACATTGCCTCCAAGATGGAGCACATGGTCTCCTCGTTCTGTCTGAAGCGCTGCAGGAGCG 2400
 342 I A S K M E H M V S S F C **L** K R C R S A 361
 2401 CCCAGGTGCTGCACCTGTATGGCGCCACCTACAGCGCGACGGGGAAGACCGCGCGAGGT 2460
 362 Q V **E** H **E** Y G A T Y S A D G E D R A R C 381
 2461 GCTCCGCGAGGAGCGCACACGCTGTTGGTGCAGCTACCAGAGAGGACCGTTCTGCTGGACG 2520
 382 S A G A H T L L V Q L P E R T V L L D A 401
 2521 CCTACAGTGAACATCTGGCAGCGGCCCTGTGCACCAATCCAAACCTGATAGAGCTGTCTC 2580
 402 Y S E H **E** A A A **E** C T N P N L I E **E** S **E** 421
 2581 TGTACCGAAATGCCCTGGGCAGCCGGGGGTGAAGCTGCTCTGTCAAGGACTCAGACACC 2640
 422 Y R N A **L** G S R G V K L **L** C Q G **E** R H P 441
 2641 CCAACTGCAAACCTCAGAACCTGAGGTAAATTTATCATATATAACATGATATTTTGAA 2700
 442 N C K **E** Q N **E** R * 449
 2701 TAAATATATTGGCCAGGTATGATGGCTCACGCCTGTAATTCAGCACTTTGGGAGGCCCA 2760
 2761 GATGGGGAGGATCACTTGACCCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCC 2820
 2821 CATCTCTACTAAAAATACCAAAATGAGCCAGGCATGGTGGCACACGTCTGTAAGCCCAGC 2880
 2881 TACTCAGGAGGCCAAGGCAGGAGGATTGCTTCAACCCAGGAGGCAGAGGTTGTGGCTGAA 2940
 2941 GAGGTGCCGCATCTCCAGCTCAGCCTGCGAGGACCTCTCTGCAGCTCTCATAGCCAATAA 3000
 3001 GAATTTGACAAGGATGGATCTCAGTGGCAACGGCGTTGGATTCCCAGGCATGATGCTGCT 3060
 3061 TTGCGAGGGCCTGCGGCATCCCCAATGCAGGCTGCAGATGATTGAGGAAGTGTCA 3120

Figure 1D

3121 GCTGGAGTCCGGGGCTTGTCTCAGGAGATGGCTTCTGTGCTTGGCACCAACCCACATCTGGT 3180
 3181 TGAGTTGGACCTGACAGGAAATGCACTGGAGGATTGGGCTGAGGTTACTATGCCAGGG 3240
 3241 ACTGAGGCACCCAGTCTGCAGACTACGGACTTTGTGGCTGAAGATCTGCCGCCTCACTGC 3300
 3301 TGCTGCCTGTGACGAGCTGGCCTCAACTCTCAGTGTGAACCAGAGCCTGAGAGAGCTGGA 3360
 3361 CCTGAGCCTGAATGAGCTGGGGGACCTCGGGGTGCTGCTGCTGTGTGAGGGCCTCAGGCA 3420
 3421 TCCCACGTGCAAGCTCCAGACCCTGCGGTGAGTCCCGTTTGTCTCACCACGCTAGGAGTC 3480
 3481 CCAATCCATGAACGCAGCCCTCTCACCTGGGACCACGGAGGCCAGGTTGTCTCTGCTCCT 3540
 3541 AAACCTCTAGCTACTACATCAGCCCTTTTTTTTTTTTTTTTGGAGACTCCCAAGTAGCTGAG 3600
 3601 ATTACAGGCGCCCGCCACCAAGCCAGCTAATTTTTTGTATTTTAGTAGAGACAGGGTT 3660
 3661 TCATCATGTTAGCAGGATGGTCTCGATCTACTGACCTCATGATCTGCCTGCCTTGGCCTC 3720
 3721 CCAAAGTGCTGGGATTACAGGCTTGAGCCACTGCACCCAGCCTACATCAGCCTTTTAA 3780
 3781 AGGATTTTTCTGGCCGGGCATGGTGGCTGACACCTTAATCCAGCACTTTTGGGAGGCCG 3840
 3841 AGGTGGGAGGATCACCTGAGGTGGGAATTCGAGACCAGCCTGACCAACATGTAGAAACA 3900
 3901 CCCCATCTGTACTAAAAATACAAAAGTAGCCAGGCATGGTGGTGCATGCCTATAATGCCA 3960
 3961 GCTACTCGCGAGGCTGAGGCAGGAGAATCCGTTGAACCCGGGAGGTGGAAGTTGCTGTGA 4020
 4021 GCTGAGATGGAGCCATTGCACTCCAGTCTGGGCAACAAGAGCGAAACTCCGCTCAAAAA 4080
 4081 AAAAAAGGGGGGGTCTTCTGACGCACGGCCCTTGCACAAGCAATTCTTATCCCTGG 4140
 4141 CATGCCTTCTGCTCTCTGTCCCCTCTTGCCTGGAGAAGTTCAATTTTCTTCTGAACAC 4200
 4201 TCTTTACTTTGTATTTTGGAGACAGGGTCTTGTCTGTCAACAGTCTGGAGTGAGTGGT 4260
 4261 GTGATCATAGCCCCGACATCCTGGGCTGAAGCCATCCTCCCAACTCAGCCTCCTGAGTAGC 4320

Figure 2A

		1	50
HNTTBMyl	(1)	-----	-----
caspase_recruitment_protein	(1)	MAAGAWGRACYLEFLKREELKEFQHLANKAHSSSSGETPAQPEKTS	SG
cryopyrin	(1)	MASTRCKLARYLEDLEVLKFKMHLLDYFQKGCPLPFRCTEKASH	
NOD1	(1)	-----MSEOGHSEMEKPSSESHPHIQLLKSNE--ELLVH	
		51	100
HNTTBMyl	(1)	-----	-----
caspase_recruitment_protein	(51)	MEVPSYLVACYGEORAPDLALHTWEOMGLRSLCAQAOEGAGHSFPYSP	
cryopyrin	(50)	UDEAPLMLDFNCEKAWANAWWIFAPLNRRDIYEKKRDEPKWCSNARV	
NOD1	(34)	LNTPCLVDN-----LLKNDYFSAEADALVACPTQPKVKRKILDLVQ	
		101	150
HNTTBMyl	(1)	-----	-----
caspase_recruitment_protein	(101)	SEPHLGSPSQPTSTAVLMPWHLPACTGSERRVLRQHTDSGRRE	
cryopyrin	(100)	SN-----PIVICOEDSEEMGLILEYLRISICKMKKDYRKVK	
NOD1	(77)	SK-----GEF--VSEFFLYLLOQADAYMDLRFWLLLEIGSP	
		151	200
HNTTBMyl	(1)	-----	-----
caspase_recruitment_protein	(151)	ISASHLYOAPSSSDHESPSQESPNAPTSTAVLGSWGSPQPQSLAPREQE	
cryopyrin	(141)	YYSRFQCIEDRNARLG-----	
NOD1	(112)	SILLQSKVYVNTLVSRYTQLR-----	
		201	250
HNTTBMyl	(1)	-----	-----
caspase_recruitment_protein	(201)	APGTQWPLDETSGIYYTEIREREREKSEKGRPPWAAVVGTPPOAHSLOP	
cryopyrin	(158)	-----	-----
NOD1	(135)	-----	-----
		251	300
HNTTBMyl	(1)	-----	-----MPKNSKVTQREH
caspase_recruitment_protein	(251)	HHHPWEPSVRESLCSTWPWKNEFDNOKFTQLLLQPHPRSQ--DPLVKRS	
cryopyrin	(158)	-----ESSLNKRYTRRLKEHRSQOEREQDLAI	
NOD1	(135)	-----HHGGRSKFVLCYAOKEELGLEIYMDIME	
		301	350
HNTTBMyl	(13)	SSEHTVESVALLALEHPVDYKQSVLNVAC-----EAG-GKQKAVSE	
caspase_recruitment_protein	(300)	WPDVVEENRCHLEIRLECEGLDTQER--IVILQGAAGTGKSTLARV	
cryopyrin	(189)	GKTKICESPVSPFKMDLLFDPDDEHSEPVH-TVVEQGAAGIGKMLARKM	
NOD1	(166)	LVCESNESSEGSINSLACLIDHTTCLNEQGETTFELGDACVGSNLLQRL	
		351	400
HNTTBMyl	(54)	ELTTERPANNKLOYLLAQIGFSVLCNWR--EPYECCKNCGAYLV	
caspase_recruitment_protein	(348)	KEAMRGCLYCDRFQHPYFSCRELAQSKVVS--TALLTGKDDTATPAE	
cryopyrin	(238)	MLDWASGTLQDRFLYFYTHCREVSVITQRS--LDDLMSCCPDNEF	
NOD1	(216)	QSLNATGRIDAG-VKLEEFRCRMFSCFKESRLQCLQDLFKHYCYFERD	
		401	450
HNTTBMyl	(101)	EYLVGLITGIFLFLPLAVGQIRRCSTGVVHYICPRLGGIGFSSQIVC	
caspase_recruitment_protein	(395)	----TROITSEPRRLFLDGVDEPGWVLEPSSBELCHMSQ--PPADAL	
cryopyrin	(285)	----THKIWRKESRLFLMDGDELOCADEHIGPLCDWQK-AARCDL	
NOD1	(265)	EEVHAFLRFPHVALFTEDGDELDHSLDLSRVEDSSCPWE--PAHPLVT	
		451	500
HNTTBMyl	(151)	LFVGLYYNVLISWSTFYFFKSFQYPLWSECPVVRNGSVAVVEACEKBS	
caspase_recruitment_protein	(440)	LSSLCKKILFEASLITARTALQNLPSLEQARWVEVLGFSESSRKEY	
cryopyrin	(330)	LSSLIRKKLLPEASLITIREVALEKLQHLHPRHVELLGFSESKRKEY	
NOD1	(314)	LANTLSGKLKCAKLEARTGTGIEVPROFLR--KKVLRGFSFSLHNAV	
		501	550
HNTTBMyl	(201)	ATTYFWYREALDISDSSESSEGTNNKTLCLLVNISTVGMAYVIGIUS-	
caspase_recruitment_protein	(490)	EYRYTDEROATRAFRVSNKELWALCLVWVWMACTCLVQMKRKE-	
cryopyrin	(380)	EYRYTDEPAQARAASLLOENVLLTTCFLVVCWLVCTGLKQOMESCK-	
NOD1	(361)	ARRMFEERALQDRLLSOLEANPNLCSSVPLFCWLTFRCEQHFRAAFEG	
		551	600
HNTTBMyl	(250)	-----GVMYFSSIFPVVLAACHLVRC-----LLLRGAV	
caspase_recruitment_protein	(539)	--KTLTTSKTTTCLNYLAQALQAP-----LGPQL	
cryopyrin	(429)	--SPAQTSKTTTAVVVFSSLLQPRGGS-----QELCLAH	
NOD1	(411)	SPQIPDCRMILTQVFLVTEVHLNRMQPSLVQRNTRSPVETILAGRITL	

[illegible][illegible]

Figure 2C

		1201	1250
	HNTTBMyl (728)	-----	-----
caspase_recruitment_protein	(1133)	DQFLGEINPQHSWMVAGPLLDIKAEPGAVEAVHLPHFVALQGQGHVDTSLF	
cryopyrin	(1035)	-----	-----
NOD1	(954)	-----	-----
		1251	1300
	HNTTBMyl (728)	-----	-----
caspase_recruitment_protein	(1183)	QVAHFKEEGMLLEKPARVELHHIVLENPSFSPLGVLLKMIHNALRFIPVT	
cryopyrin	(1035)	-----	-----
NOD1	(954)	-----	-----
		1301	1350
	HNTTBMyl (728)	-----	-----
caspase_recruitment_protein	(1233)	SVVLLYHRLHPPEEVTFHLYLIPSDCSIRKELELCYRSPGEDQLFSEFYVG	
cryopyrin	(1035)	-----	-----
NOD1	(954)	-----	-----
		1351	1400
	HNTTBMyl (728)	-----	-----
caspase_recruitment_protein	(1283)	HLGSGIRLQVKDKKDETLVWEALVKPGDLMPATTLIPACIAVPSPLDAP	
cryopyrin	(1035)	-----	-----
NOD1	(954)	-----	-----
		1401	1450
	HNTTBMyl (728)	-----	-----
caspase_recruitment_protein	(1333)	QLLHFVDQYREQLIARVTSVEVVLDKLHGQVLSQEYQYERVLAENTRPSQM	
cryopyrin	(1035)	-----	-----
NOD1	(954)	-----	-----
		1451	1497
	HNTTBMyl (728)	-----	-----
caspase_recruitment_protein	(1383)	RKLFSLSQSWDRKCKDGLYQALKETHPHLIMELWEKGSKKGLLPLSS	
cryopyrin	(1035)	-----	-----
NOD1	(954)	-----	-----

Figure 3

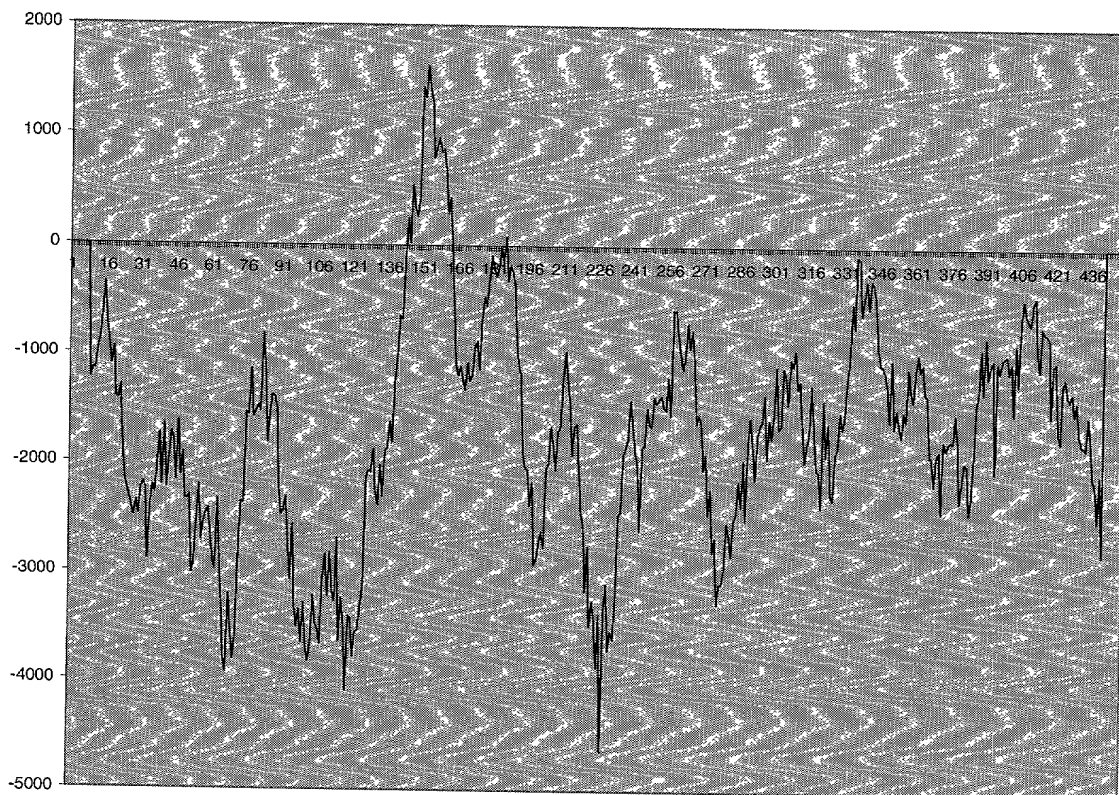


Figure 4

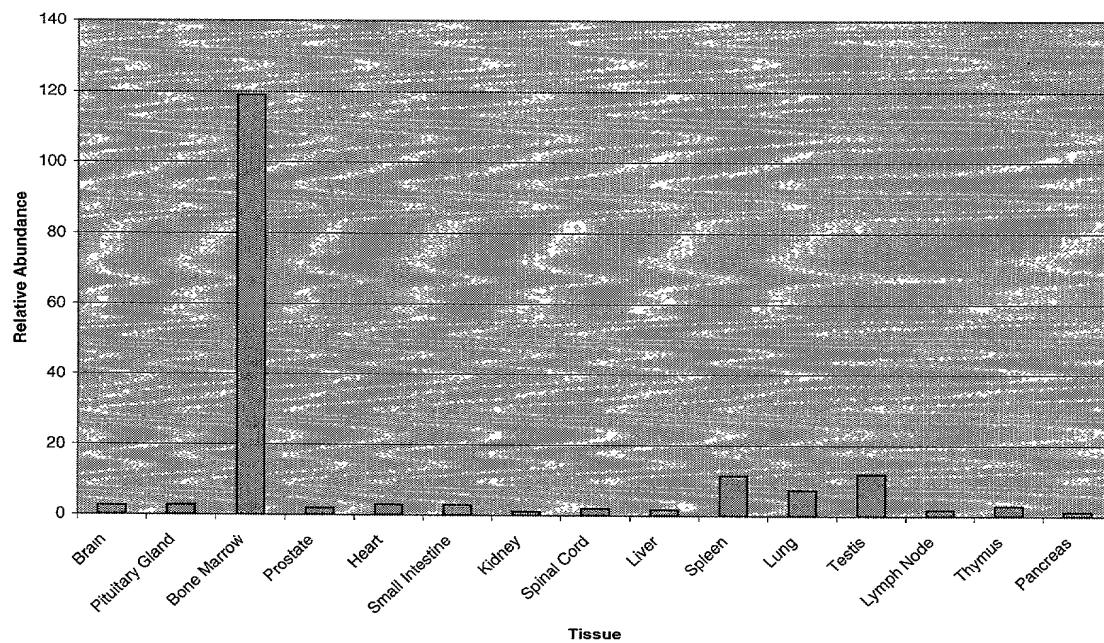


Figure 5.

<u>Protein</u>	<u>Genbank ID</u>	<u>Percent Identity</u>	<u>Percent Similarity</u>
human caspase recruitment protein 7	gil10198209	35%	48%
human NOD caspase recruitment protein 4	gil5174617	25%	38%
human cryopyrin protein	gil17027237	51.7%	64.0%